



1600

## RAW SEQUENCE LISTING

DATE: 04/08/2004

PATENT APPLICATION: US/09/686,346B

TIME: 16:10:19

Input Set : D:\Utsd1276.app

Output Set: N:\CRF4\04082004\I686346B.raw

3 <110> APPLICANT: COBB, MELANIE  
 4 HUTCHISON, MICHELE  
 5 ZHU, CHEN  
 6 BERMAN, KEVIN  
 8 <120> TITLE OF INVENTION: TAO PROTEIN KINASE POLYPEPTIDES AND METHODS OF UE  
 9 THEREFOR  
 11 <130> FILE REFERENCE: UTSD:1276USC1  
 13 <140> CURRENT APPLICATION NUMBER: 09/686,346B  
 14 <141> CURRENT FILING DATE: 2000-10-10  
 16 <150> PRIOR APPLICATION NUMBER: 09/060,410  
 17 <151> PRIOR FILING DATE: 1998-04-14  
 19 <160> NUMBER OF SEQ ID NOS: 28  
 21 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 3312  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Rattus norvegicus  
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 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (121)..(3123)  
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 37 atg cca tca act aac aga gca ggc agt cta aag gac cct gaa atc gca 168  
 38 Met Pro Ser Thr Asn Arg Ala Gly Ser Leu Lys Asp Pro Glu Ile Ala  
 39 1 5 10 15  
 41 gag ctg ttc ttc aaa gaa gat ccg gaa aaa ctg ttc aca gat ctg aga 216  
 42 Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe Thr Asp Leu Arg  
 43 20 25 30  
 45 gaa atc ggc cat ggg agc ttt gga gca gtt tat ttt gca cga gat gtg 264  
 46 Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val  
 47 35 40 45  
 49 cgt act aat gaa gtg gtg gcc atc aag aaa atg tct tat agt gga aag 312  
 50 Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys  
 51 50 55 60  
 53 cag tct act gag aaa tgg cag gat att att aag gaa gtc aag ttt cta 360  
 54 Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu  
 55 65 70 75 80  
 57 caa aga ata aaa cat ccc aac agt ata gaa tac aaa ggc tgc tat tta 408  
 58 Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu  
 59 85 90 95  
 61 cgt gaa cac aca gca tgg ctt gta atg gaa tat tgt tta gga tct gct 456  
 62 Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala

pg. 6  
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67	115 120 125			
69	gca gca att aca cat ggt gct ctc cag gga tta gct tat tta cat tct	552		
70	Ala Ala Ile Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser			
71	130 135 140			
73	cat acc atg atc cat aga gat atc aaa gca gga aat atc ctt ctg aca	600		
74	His Thr Met Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr			
75	145 150 155 160			
77	gaa cca ggc caa gtg aaa ctt gct gac ttt gga tct gct tcc atg gcc	648		
78	Glu Pro Gly Gln Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Met Ala			
79	165 170 175			
81	tcc cct gcc aat tct ttt gtg gga aca cca tat tgg atg gcc cca gaa	696		
82	Ser Pro Ala Asn Ser Phe Val Gly Thr Pro Tyr Trp Met Ala Pro Glu			
83	180 185 190			
85	gta att tta gcc atg gat gaa gga caa tat gat ggc aaa gtt gat gta	744		
86	Val Ile Leu Ala Met Asp Glu Gly Gln Tyr Asp Gly Lys Val Asp Val			
87	195 200 205			
89	tgg tct ctt gga ata aca tgt att gaa tta gcc gag agg aag cct cct	792		
90	Trp Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Lys Pro Pro			
91	210 215 220			
93	tta ttt aat atg aat gca atg agt gcc tta tat cac ata gcc caa aat	840		
94	Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn			
95	225 230 235 240			
97	gaa tcc cct aca cta cag tct aat gaa tgg tct gat tat ttt cga aac	888		
98	Glu Ser Pro Thr Leu Gln Ser Asn Glu Trp Ser Asp Tyr Phe Arg Asn			
99	245 250 255			
101	ttt gta gat tct tgc ctc cag aaa atc cct caa gat cgc cct aca tca	936		
102	Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg Pro Thr Ser			
103	260 265 270			
105	gag gaa ctt tta aag cac atg ttt gtt ctt cga gag cgc cct gaa aca	984		
106	Glu Glu Leu Leu Lys His Met Phe Val Leu Arg Glu Arg Pro Glu Thr			
107	275 280 285			
109	gtg tta ata gat ctt att caa agg aca aag gat gca gta aga gag ctg	1032		
110	Val Leu Ile Asp Leu Ile Gln Arg Thr Lys Asp Ala Val Arg Glu Leu			
111	290 295 300			
113	gac aat cta caa tat cga aag atg aag aaa ctc ctt ttc cag gag gca	1080		
114	Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Leu Leu Phe Gln Glu Ala			
115	305 310 315 320			
117	cat aat gga cca gca gta gaa gca cag gaa gaa gag gag gag caa gat	1128		
118	His Asn Gly Pro Ala Val Glu Ala Gln Glu Glu Glu Glu Glu Asp			
119	325 330 335			
121	cat ggt ggt ggc cgg aca gga aca gta aat agt gtt gga agc aat cag	1176		
122	His Gly Gly Gly Arg Thr Gly Thr Val Asn Ser Val Gly Ser Asn Gln			
123	340 345 350			
125	tct atc ccc agt atg tct atc agt gcc agt agc caa agc agc agt gtt	1224		
126	Ser Ile Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser Ser Ser Val			
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129	aat	agt	ctt	cca	gat	gca	tcg	gat	gac	aag	agt	gag	cta	gac	atg	atg	1272
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131		370					375					380					
133	gag	gga	gac	cat	aca	gtg	atg	tct	aac	agt	tct	gtc	atc	cac	tta	aaa	1320
134	Glu	Gly	Asp	His	Thr	Val	Met	Ser	Asn	Ser	Ser	Val	Ile	His	Leu	Lys	
135	385					390					395					400	
137	cct	gag	gag	gaa	aat	tac	caa	gaa	gaa	gga	gat	cct	aga	aca	aga	gca	1368
138	Pro	Glu	Glu	Glu	Asn	Tyr	Gln	Glu	Glu	Gly	Asp	Pro	Arg	Thr	Arg	Ala	
139					405					410						415	
141	tca	gct	cca	cag	tct	cca	cct	caa	gtg	tct	cgt	cac	aaa	tca	cat	tat	1416
142	Ser	Ala	Pro	Gln	Ser	Pro	Pro	Gln	Val	Ser	Arg	His	Lys	Ser	His	Tyr	
143				420					425							430	
145	cgt	aat	aga	gaa	cac	ttt	gca	act	ata	cga	aca	gca	tca	ctg	gtt	aca	1464
146	Arg	Asn	Arg	Glu	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	Ser	Leu	Val	Thr	
147				435					440							445	
149	aga	cag	atg	caa	gaa	cat	gag	cag	gac	tct	gaa	ctt	aga	gaa	cag	atg	1512
150	Arg	Gln	Met	Gln	Glu	His	Glu	Gln	Asp	Ser	Glu	Leu	Arg	Glu	Gln	Met	
151				450					455							460	
153	tct	ggt	tat	aag	cgg	atg	agg	cga	cag	cat	cag	aag	cag	ctg	atg	act	1560
154	Ser	Gly	Tyr	Lys	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Met	Thr	
155	465				470						475					480	
157	ctg	gaa	aat	aaa	ctg	aag	gca	gaa	atg	gac	gaa	cat	cgg	ctc	aga	tta	1608
158	Leu	Glu	Asn	Lys	Leu	Lys	Ala	Glu	Met	Asp	Glu	His	Arg	Leu	Arg	Leu	
159				485							490					495	
161	gac	aaa	gat	ctt	gaa	act	cag	cgc	aac	aat	ttc	gct	gca	gaa	atg	gag	1656
162	Asp	Lys	Asp	Leu	Glu	Thr	Gln	Arg	Asn	Asn	Phe	Ala	Ala	Glu	Met	Glu	
163				500					505							510	
165	aaa	ctt	att	aag	aaa	cac	caa	gct	tct	atg	gaa	aaa	gag	gct	aaa	gtg	1704
166	Lys	Leu	Ile	Lys	Lys	His	Gln	Ala	Ser	Met	Glu	Lys	Glu	Ala	Lys	Val	
167				515					520							525	
169	atg	gcc	aac	gag	gag	aaa	aaa	ttc	caa	caa	cac	att	cag	gct	caa	cag	1752
170	Met	Ala	Asn	Glu	Glu	Lys	Lys	Phe	Gln	Gln	His	Ile	Gln	Ala	Gln	Gln	
171				530					535							540	
173	aag	aaa	gaa	ctg	aat	agc	ttt	ttg	gag	tct	caa	aaa	aga	gaa	tat	aaa	1800
174	Lys	Lys	Glu	Leu	Asn	Ser	Phe	Leu	Glu	Ser	Gln	Lys	Arg	Glu	Tyr	Lys	
175	545					550					555					560	
177	ctt	cga	aaa	gag	cag	ctt	aag	gag	gag	ctg	aat	gaa	aac	cag	agc	aca	1848
178	Leu	Arg	Lys	Glu	Gln	Leu	Lys	Glu	Glu	Leu	Asn	Glu	Asn	Gln	Ser	Thr	
179					565					570						575	
181	cct	aaa	aaa	gaa	aag	cag	gaa	tgg	ctt	tca	aag	cag	aag	gag	aat	att	1896
182	Pro	Lys	Lys	Glu	Lys	Gln	Glu	Trp	Leu	Ser	Lys	Gln	Lys	Glu	Asn	Ile	
183				580					585							590	
185	caa	cat	ttt	cag	gca	gaa	gaa	gaa	gct	aat	ctt	ctt	cga	cgt	caa	agg	1944
186	Gln	His	Phe	Gln	Ala	Glu	Glu	Glu	Ala	Asn	Leu	Leu	Arg	Arg	Gln	Arg	
187				595					600							605	
189	cag	tat	cta	gag	cta	gaa	tgt	cgt	cgc	ttc	aaa	aga	aga	atg	tta	ctt	1992
190	Gln	Tyr	Leu	Glu	Leu	Glu	Cys	Arg	Arg	Phe	Lys	Arg	Arg	Met	Leu	Leu	
191				610					615							620	
193	ggt	cgg	cat	aac	ttg	gaa	cag	gac	ctt	gtc	agg	gag	gag	tta	aac	aaa	2040

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194	Gly	Arg	His	Asn	Leu	Glu	Gln	Asp	Leu	Val	Arg	Glu	Glu	Leu	Asn	Lys	
195	625					630					635					640	
197	agg	cag	act	cag	aag	gac	tta	gaa	cat	gca	atg	tta	ctg	cga	cag	cat	2088
198	Arg	Gln	Thr	Gln	Lys	Asp	Leu	Glu	His	Ala	Met	Leu	Leu	Arg	Gln	His	
199				645						650					655		
201	gaa	tcc	atg	caa	gaa	ctg	gag	ttt	cgc	cac	ctc	aac	act	att	cag	aag	2136
202	Glu	Ser	Met	Gln	Glu	Leu	Glu	Phe	Arg	His	Leu	Asn	Thr	Ile	Gln	Lys	
203				660					665						670		
205	atg	cgc	tgt	gag	ttg	atc	aga	ctg	caa	cat	caa	act	gag	ctt	act	aac	2184
206	Met	Arg	Cys	Glu	Leu	Ile	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Thr	Asn	
207			675				680							685			
209	cag	ctg	gaa	tac	aat	aag	aga	agg	gaa	cgg	gaa	cta	aga	cgg	aaa	cat	2232
210	Gln	Leu	Glu	Tyr	Asn	Lys	Arg	Arg	Glu	Arg	Glu	Leu	Arg	Arg	Lys	His	
211		690					695					700					
213	gtc	atg	gaa	gtt	cga	cag	cag	cct	aag	agt	ttg	aag	tct	aaa	gaa	ctc	2280
214	Val	Met	Glu	Val	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Ser	Lys	Glu	Leu	
215	705					710					715				720		
217	caa	ata	aaa	aag	cag	ttt	cag	gat	acc	tgc	aaa	att	caa	acc	aga	cag	2328
218	Gln	Ile	Lys	Lys	Gln	Phe	Gln	Asp	Thr	Cys	Lys	Ile	Gln	Thr	Arg	Gln	
219				725					730						735		
221	tac	aaa	gca	tta	agg	aat	cac	cta	ctg	gag	act	aca	cca	aag	agt	gag	2376
222	Tyr	Lys	Ala	Leu	Arg	Asn	His	Leu	Leu	Glu	Thr	Thr	Pro	Lys	Ser	Glu	
223				740					745					750			
225	cac	aaa	gct	gtt	ctg	aaa	aga	ctc	aag	gag	gaa	cag	act	cgg	aag	tta	2424
226	His	Lys	Ala	Val	Leu	Lys	Arg	Leu	Lys	Glu	Glu	Gln	Thr	Arg	Lys	Leu	
227			755					760					765				
229	gcc	atc	ttg	gct	gag	cag	tat	gat	cat	agc	att	aat	gaa	atg	ctc	tcc	2472
230	Ala	Ile	Leu	Ala	Glu	Gln	Tyr	Asp	His	Ser	Ile	Asn	Glu	Met	Leu	Ser	
231		770				775						780					
233	aca	caa	gct	ctg	cgt	ttg	gat	gaa	gca	cag	gaa	gca	gaa	tgc	cag	gtt	2520
234	Thr	Gln	Ala	Leu	Arg	Leu	Asp	Glu	Ala	Gln	Glu	Ala	Glu	Cys	Gln	Val	
235	785				790					795					800		
237	ttg	aag	atg	cag	cta	cag	cag	gaa	ctg	gag	ctg	ttg	aat	gca	tat	cag	2568
238	Leu	Lys	Met	Gln	Leu	Gln	Gln	Glu	Leu	Glu	Leu	Leu	Asn	Ala	Tyr	Gln	
239				805					810						815		
241	agc	aaa	atc	aag	atg	cag	gct	gag	gcc	caa	cat	gat	cga	gag	ctt	cga	2616
242	Ser	Lys	Ile	Lys	Met	Gln	Ala	Glu	Ala	Gln	His	Asp	Arg	Glu	Leu	Arg	
243				820					825					830			
245	gag	ctg	gaa	caa	agg	gtc	tcc	ctt	cgg	aga	gca	ctc	tta	gaa	cag	aag	2664
246	Glu	Leu	Glu	Gln	Arg	Val	Ser	Leu	Arg	Arg	Ala	Leu	Leu	Glu	Gln	Lys	
247			835					840						845			
249	att	gaa	gaa	gag	atg	ttg	gct	ttg	cag	aat	gaa	cgc	aca	gaa	cga	ata	2712
250	Ile	Glu	Glu	Glu	Met	Leu	Ala	Leu	Gln	Asn	Glu	Arg	Thr	Glu	Arg	Ile	
251		850				855						860					
253	cgt	agc	ctg	ctc	gag	cgc	cag	gcc	aga	gaa	att	gaa	gct	ttt	gac	tct	2760
254	Arg	Ser	Leu	Leu	Glu	Arg	Gln	Ala	Arg	Glu	Ile	Glu	Ala	Phe	Asp	Ser	
255	865				870					875					880		
257	gaa	agc	atg	aga	tta	ggt	ttt	agt	aac	atg	gtc	ctt	tct	aat	ctc	tcc	2808
258	Glu	Ser	Met	Arg	Leu	Gly	Phe	Ser	Asn	Met	Val	Leu	Ser	Asn	Leu	Ser	

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261 cct gag gca ttc agc cac agc tac cca gga gct tct agc tgg tct cac 2856
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263          900          905          910
265 aat cct act ggg ggt tca gga cct cac tgg ggt cat ccc atg ggt ggc 2904
266 Asn Pro Thr Gly Gly Ser Gly Pro His Trp Gly His Pro Met Gly Gly
267          915          920          925
269 aca cca caa gct tgg ggt cat ccg atg caa ggc gga ccc caa cca tgg 2952
270 Thr Pro Gln Ala Trp Gly His Pro Met Gln Gly Gly Pro Gln Pro Trp
271          930          935          940
273 ggt cac ccc tca ggg cca atg caa ggg gta cct cga ggt agc agt ata 3000
274 Gly His Pro Ser Gly Pro Met Gln Gly Val Pro Arg Gly Ser Ser Ile
275 945          950          955          960
277 gga gtc cgc aat agc ccc cag gct ctg agg cgg aca gct tct ggg gga 3048
278 Gly Val Arg Asn Ser Pro Gln Ala Leu Arg Arg Thr Ala Ser Gly Gly
279          965          970          975
281 cgg acg gaa cag ggc atg agc aga agc acg agt gtc act tca caa ata 3096
282 Arg Thr Glu Gln Gly Met Ser Arg Ser Thr Ser Val Thr Ser Gln Ile
283          980          985          990
285 tcc aat ggg tca cac atg tct tac aca taataattga aagtggcaat 3143
286 Ser Asn Gly Ser His Met Ser Tyr Thr
287          995          1000
289 tccgctggag ctgtctgccaa aaagaaactg cctacagaca tcagcacagc agcctcctca 3203
291 cttgggtact accgggtgga agctgtgcat atggtatatt ttattcgtct ttgtaaagcg 3263
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308 Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
309 35 40 45
311 Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
312 50 55 60
314 Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu
315 65 70 75 80
317 Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu
318 85 90 95
320 Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
321 100 105 110
323 Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile
324 115 120 125
326 Ala Ala Ile Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser
327 130 135 140
329 His Thr Met Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:7; N Pos. 208,210,223  
Seq#:10; N Pos. 192  
Seq#:11; N Pos. 18  
Seq#:19; N Pos. 24,31  
Seq#:20; N Pos. 3,6,13,16,19  
Seq#:21; N Pos. 11,14,18  
Seq#:22; N Pos. 19,22

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L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

M:341 Repeated in SeqNo=5

L:1049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:180

L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:180

L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

L:1296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0

L:1314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0

L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0

L:1350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0